

Amendments to the Claims:

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

Claim 1 (currently amended) A method for the simultaneous quantitative analysis of at least three samples of molecules, comprising:

- (i) reacting the molecules of each sample with ~~a set of~~ at least two ~~isotopically labelled~~ differential isotope labeled reagents, wherein ~~each set of isotopically labelled~~ the reagents is differentially labelled, resulting in at least three differentially and isotopically labelled are directly labeled, and wherein the differential isotope labeled reagents result in differential isotope labeled derivatives of molecules;
- (ii) combining the ~~derivatized molecules in a preparation~~ derivatives for examination by mass spectrometry; and
- (iii) examining the ~~preparation~~ derivatives by mass spectrometry.

Claim 2 (currently amended) A method for the quantitative analysis of a sample of molecules having an amine bearing an active hydrogen, comprising:

- (i) reacting the molecules, with ~~isotopically labelled reagents resulting in the~~ differential isotope labeled reagents, wherein the reagents are directly labeled, and wherein the differential isotope labeled reagents results in a reductive alkylation of the amines amine to their its alkylamine derivatives derivative, such that the alkylamine ~~derivatives are derivative is~~ isotopically labelled in a preparation labeled for examination by mass spectrometry; and
- (ii) examining the ~~preparation~~ derivative by mass spectrometry.

Claim 3 (currently amended) A method for the quantitative analysis of two or more samples of molecules having an amine bearing an active hydrogen, comprising:

- (i) reacting the molecules in each sample with ~~isotopically labelled reagents resulting in the differential isotope labeled reagents~~, wherein the reagents are directly labeled, and wherein the differential isotope labeled reagents result in a reductive alkylation of the ~~amines-amine~~ to ~~their-its~~ alkylamine ~~derivatives-derivative~~, such that the alkylamine derivatives are ~~isotopically labelled-differentially isotopically labeled~~;
- (ii) combining the ~~derivatized molecules in a preparation~~ derivatives for examination by mass spectrometry; and
- (iii) examining the ~~preparation-derivatives~~ by mass spectrometry.

Claim 4 (currently amended) The method of claim 1, 2 or 3 comprising an additional step of cleaving the ~~derivatized molecules in the preparation-derivatives~~ into fragments, prior to the step of examining the ~~preparation-derivatives~~ by mass spectrometry.

Claim 5 (currently amended) The method of claim 1, 2 or 3 comprising an additional step of denaturing the molecules prior to the step of reacting the molecules with ~~isotopically labelled-differential isotope labeled~~ reagents.

Claim 6 (currently amended) The method of claim 1, 2, 3 or 4 wherein the step of examining the ~~preparation-derivatives~~ by mass spectrometry comprises introducing the ~~preparation containing the derivatized molecules-derivatives~~ or fragments to a mass spectrometer using electrospray ionization ~~ionisation~~.

Claim 7 (currently amended) The method of claim 6 wherein the electrospray ionization ~~ionisation~~ method is selected from a group consisting of nanospray, pneumatically assisted electrospray, ionspray and turboionspray.

Claim 8 (currently amended) The method of claim 1, 2 or 3 comprising an additional step of separating the ~~derivatized molecules in the preparation-derivatives~~ before the step of examining the ~~preparation-derivatives~~ by mass spectrometry.

Claim 9 (currently amended) The method of claim 8 wherein the step of separating the ~~derivatized molecules~~ derivatives uses a separator selected from a group consisting of 1-D gel electrophoresis, SDS-PAGE, isoelectric focusing, 2-D gel electrophoresis, zone electrophoresis, isotachopheresis, ion exchange chromatography, normal phase chromatography, reverse phase chromatography, hydrophobic interaction chromatography, size exclusion chromatography and any combination of these separators.

Claim 10 (currently amended) The method of claim 4 comprising an additional step of separating the fragments after the step of cleaving the ~~derivatized molecules in the preparation~~ derivatives and before the step of examining the derivatives.

Claim 11 (original) The method of claim 10 wherein the step of separating the fragments uses a separator selected from a group consisting of liquid chromatography, high performance liquid chromatography and capillary electrophoresis.

Claim 12 (currently amended) The method of claims 1, 2 or 3 comprising an additional step of analyzing the ~~preparation derivatives~~ after the step of examining the preparation derivatives by mass spectrometry.

Claim 13 (currently amended) The method of claim 12 wherein the derivatives are peptides and the step of analyzing the ~~preparation derivatives~~ is selected from a group consisting of collision-induced dissociation in a mass spectrometer operating in MS/MS mode, peptide mass fingerprinting, peptide mapping, Edman sequencing and sequencing by sequential amino acid cleavage.

Claim 14 (currently amended) The method of claim 13, comprising an additional step, after the step of analyzing the ~~preparation derivatives~~, of sequencing the molecule.

Claim 15 (currently amended) The method of claim 1, 2 or 3 wherein the ~~isotopically labelled~~ differential isotope labeled reagents are an aldehyde and a reducing agent.

Claim 16 (original) The method of claim 15 wherein the aldehyde is selected from a group consisting of formaldehyde and acetaldehyde.

Claim 17 (original) The method of claim 15 wherein the reducing agent is selected from a group consisting of a sodium cyanoborohydride, sodium borohydride, dialkyl borane complexes and pyridine borane complexes.

Claim 18 (currently amended) The method of claim 1, 2 or 3 wherein the sample in any one of claim 1, 2 or 3 is selected from a group consisting of cells, cellular extracts, sub-cellular extracts, cellular lysates, peptides, proteins, drugs, toxins, antibodies and pollutants.

Claim 19 (original) The method of claim 18 wherein the proteins are extracted from cells.

Claim 20 (currently amended) The method of claim 19 wherein the ~~amines-amine~~ of the proteins ~~are-is~~ selected from a group consisting of a lysine residues-residue, ornithine ~~residues-residue~~ and ~~residues~~ a residue at the N- terminal amino group of the proteins.

Claim 21 (currently amended) The method of claim 1, 2 or 3 wherein the step of examining the ~~preparation-derivatives~~ by mass spectrometry utilizes a mass spectrometer selected from a group consisting of:

- (i) Fourier transform – Ion cyclotron resonance mass spectrometers (FT-ICR-MS);
- (ii) Time of Flight mass spectrometers (TOF-MS, TOF-TOF-MS);
- (iii) Ion trap mass spectrometers (IT);
- (iv) Quadrupole mass spectrometers (Q-MS and QqQ-MS);
- (v) Ion mobility mass spectrometers (IM-MS);
- (vi) Quadrupole (or hexapole, octapole)-Time of Flight mass spectrometers (Q-TOF, and Qq-TOF); and
- (vii) Ion trap – Time of flight mass spectrometers (IT-TOF).

Claim 22 (currently amended) The method of claim 21 comprising an additional step of combining the mass spectrometer with an ionization ~~ionisation~~ source.

- Claim 23 (currently amended) The method of claim 22 wherein the ionization ~~ionisation~~ source is selected from a group consisting of electrospray ionization ~~ionisation~~, matrix-assisted laser desorption and ionization ~~ionisation~~ (MALDI), field desorption, thermal desorption and laser desorption.
- Claim 24 (currently amended) A preparation ~~of comprising~~ three samples of molecules for simultaneous quantitative analysis by mass spectrometry, each sample comprising ~~differentially and isotopically labelled~~ labeled derivatives of molecules, each sample resulting from a reaction of ~~a set of at least two isotopically labelled~~ differential isotope labeled reagents with the molecules, wherein the reagents are directly labeled.
- Claim 25 (currently amended) A preparation ~~of comprising~~ a sample of molecules having an amine bearing an active hydrogen, comprising isotopically ~~labelled~~ labeled derivatives resulting from ~~the a~~ reductive alkylation of the ~~amines~~ amine to its alkylamine ~~derivatives~~ derivative by ~~isotopically labelled~~ differential isotope labeled reagents, wherein the reagents are directly labeled.
- Claim 26 (currently amended) A preparation ~~of comprising~~ two or more samples of molecules having an amine bearing an active hydrogen, for the simultaneous analysis by mass spectrometry, each sample comprising ~~differentially and isotopically labelled~~ labeled derivatives of molecules resulting from ~~the a~~ reductive alkylation of the ~~amines~~ amine to its alkylamine ~~derivatives~~ derivative by ~~isotopically labelled~~ differential isotope labeled reagents, wherein the reagents are directly labeled.
- Claim 27 (currently amended) Use of a mass spectrometer for the analysis of a sample according to the steps recited in any one of claims 1, 2 or 3.
- Claim 28 (withdrawn) A kit comprising ~~isotopically labelled~~ differential isotope labeled reagents and instructions to follow the methods of quantitative analysis of any of claims 1, 2 or 3.

Claim 29 (currently amended) A method for the quantitative analysis of two or more cellular extracts comprising molecules having an amine bearing an active hydrogen, comprising:

- (i) reacting the molecules of the extracts with ~~isotopically labelled~~ differential isotope labeled reagents, ~~wherein the reagents are directly labeled,~~ resulting in ~~the a~~ reductive alkylation of the ~~amines-amine~~ to ~~their-its~~ alkylamine ~~derivatives-derivative~~, such that the alkylamine derivatives are isotopically ~~labelled~~ labeled;
- (ii) combining the ~~derivatized molecules-derivatives~~ of the extracts ~~in a preparation~~;
- (iii) separating the ~~molecules-derivatives~~;
- (iv) enzymatically cleaving the ~~molecules-derivatives~~ into fragments;
- (v) separating the fragments;
- (vi) examining the fragments by mass spectrometry; and
- (vii) sequencing the fragments.